

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Goli, Surya K.
Hillman, Jennifer L.
- (ii) TITLE OF THE INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0187 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Consensus
 - (B) CLONE: Consensus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Ala Ala Ala Ala Val Ala Arg Leu Trp Trp Arg Gly Ile Leu Gly
 1 5 10 15
 Ala Ser Ala Leu Thr Arg Gly Thr Gly Arg Pro Ser Val Leu Leu Leu
 20 25 30
 Pro Val Arg Arg Glu Ser Ala Gly Ala Asp Thr Arg Pro Thr Val Arg
 35 40 45
 Pro Arg Asn Asp Val Ala His Lys Gln Leu Ser Ala Phe Gly Glu Tyr
 50 55 60
 Val Ala Glu Ile Leu Pro Lys Tyr Val Gln Gln Val Gln Val Ser Cys
 65 70 75 80
 Phe Asn Glu Leu Glu Val Cys Ile His Pro Asp Gly Val Ile Pro Val
 85 90 95
 Leu Thr Phe Leu Arg Asp His Thr Asn Ala Gln Phe Lys Ser Leu Val
 100 105 110
 Asp Leu Thr Ala Val Asp Val Pro Thr Arg Gln Asn Arg Phe Glu Ile
 115 120 125
 Val Tyr Asn Leu Leu Ser Leu Arg Phe Asn Ser Arg Ile Arg Val Lys
 130 135 140
 Thr Tyr Thr Asp Glu Leu Thr Pro Ile Glu Ser Ala Val Ser Val Phe
 145 150 155 160
 Lys Ala Ala Asn Trp Tyr Glu Arg Glu Ile Trp Asp Met Phe Gly Val
 165 170 175
 Phe Phe Ala Asn His Pro Asp Leu Arg Arg Ile Leu Thr Asp Tyr Gly
 180 185 190
 Phe Glu Gly His Pro Phe Arg Lys Asp Phe Pro Leu Ser Gly Tyr Val
 195 200 205
 Glu Leu Arg Tyr Asp Asp Glu Val Lys Arg Val Val Ala Glu Pro Val
 210 215 220
 Glu Leu Ala Gln Glu Phe Arg Lys Phe Asp Leu Asn Ser Pro Trp Glu
 225 230 235 240
 Ala Phe Pro Val Tyr Arg Gln Pro Pro Glu Ser Leu Lys Leu Glu Ala
 245 250 255
 Gly Asp Lys Lys Pro Asp Ala Lys
 260

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAACTCTAAT	ACGAGCACTA	TAGGGAAAGC	TGGTAGCCTG	CAGGTACCGG	TCCGGAATTC	60
CCGGGTGCGAC	CCACGCGTCC	GCCGTGCCCT	TGGGGCTCCG	TGTCCTGCTG	TCTTTCCGTC	120
CGCTGCCTAG	TCTGCATCTG	AGTAACATGG	CGGCGGCGGC	GGTAGCCAGG	CTGTGGTGGC	180
GCGGGATCTT	GGGGGCTCG	GCGCTGACCA	GGGGGACTGG	GCGACCCTCC	GTTCTGTTGC	240
TGCCGGTGAG	GCGGGAGAGC	GCCGGGGCCG	ACACGCGCCC	CACTGTCAGA	CCACGGAATG	300
ATGTGGCCCA	CAAGCAGCTC	TCAGCTTTTG	GAGAGTATGT	GGCTGAAATC	TTGCCCAAGT	360
ATGTCCAACA	AGTTCAGGTG	TCCTGCTTCA	ATGAGTTAGA	GGTCTGTATC	CATCCTGATG	420
GCGTCATCCC	AGTGCTGACT	TTCTCAGGG	ATCACACCAA	TGCACAGTTC	AAATCTCTGG	480
TTGACTTGAC	AGCAGTGGAC	GTCCCAACTC	GGCAAAACCG	TTTTGAGATT	GTCTACAACC	540
TGTTGTCTCT	GCGCTTCAAC	TCACGGATCC	GTGTGAAGAC	CTACACAGAT	GAGCTGACGC	600
CCATTGAGTC	TGCTGTCTCT	GTGTTCAAGG	CAGCCAACTG	GTATGAAAGG	GAGATCTGGG	660
ACATGTTTGG	AGTCTTCTTT	GCTAACCACC	CTGATCTAAG	AAGGATCCTG	ACAGATTATG	720

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GCTTCGAGGG ACATCCTTTC CGGAAAGACT TTCCTCTATC TGGCTATGTT GAGTTACGTT 780
ATGATGATGA AGTGAAGCGT GTGGTGGCAG AGCCGGTGGA GTTGGCCCAA GAGTTCCGCA 840
AATTTGACCT GAACAGCCCC TGGGAGGCTT TCCCAGTCTA TCGCCAACCC CCGGAGAGTC 900
TCAAGCTTGA AGCCGGAGAC AAGAAGCCTG ATGCCAAGTA GCTCCAGGGA ACGCATGTGG 960
ATCCTAGACA GCGCCTTATC TATGATTGAG TGTCCGTGTA AATAAATTC TACTTAGACT 1020
TAC 1023

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Phe Pro Lys Tyr Lys Pro Ser Ser Leu Arg Thr Leu Pro Glu
1 5 10 15
Thr Leu Asp Pro Ala Glu Tyr Asn Ile Ser Pro Glu Thr Arg Arg Ala
20 25 30
Gln Ala Glu Arg Leu Ala Ile Arg Ala Gln Leu Lys Arg Glu Tyr Leu
35 40 45
Leu Gln Tyr Asn Asp Pro Asn Arg Arg Gly Leu Ile Glu Asn Pro Ala
50 55 60
Leu Leu Arg Trp Ala Tyr Ala Arg Thr Ile Asn Val Tyr Pro Asn Phe
65 70 75 80
Arg Pro Thr Pro Lys Asn Ser Leu Met Gly Ala Leu Cys Gly Phe Gly
85 90 95
Pro Leu Ile Phe Ile Tyr Tyr Ile Ile Lys Thr Glu Arg Asp Arg Lys
100 105 110
Glu Lys Leu Ile Gln Glu Gly Lys Leu Asp Arg Thr Phe His Leu Ser
115 120 125
Tyr

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCAAGATGTC GTTCCCAAAG TATAAGCCGT CGAGCCTGCG CACTCTGCCT GAGACCCTCG 60
ACCCAGCCGA ATACAACATA TCTCCGAAA CCCGGCGGGC GCAAGCGGAG CGGTTGGCCA 120
TAAGAGCCCA GCTGAAACGA GAGTACCTGC TTCAGTACAA CGATCCCAAC CGCCGAGGGC 180
TCATCGAAAA TCCTGCCCTG CTTCGTTGGG CCTATGCAAG AACAATAAAT GTCTATCCTA 240
ATTTCAAGACC CACTCCTAAA AACTCACTCA TGGGAGCTCT GTGTGGATTT GGGCCCCTCA 300
TCTTCATTTA TTATATTATC AAAACTGAGA GGGATAGGAA AGAAAACTT ATCCAGGAAG 360
GAAAATTGGA TCGAACATTT CACCTCTCAT ATTAAGTCTG GCAATGATGA CTATATGTAT 420

TCCTGCCTAA ATAAATCATC TATTAATCAT T

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Pro	Phe	Leu	Asp	Ile	Gln	Lys	Arg	Phe	Gly	Leu	Asn	Ile	Asp	Arg
1				5					10					15	
Trp	Leu	Thr	Ile	Gln	Ser	Gly	Glu	Gln	Pro	Tyr	Lys	Met	Ala	Gly	Arg
			20					25					30		
Cys	His	Ala	Phe	Glu	Lys	Glu	Trp	Ile	Glu	Cys	Ala	His	Gly	Ile	Gly
		35					40					45			
Tyr	Thr	Arg	Ala	Glu	Lys	Glu	Cys	Lys	Ile	Glu	Tyr	Asp	Asp	Phe	Val
	50					55					60				
Glu	Cys	Leu	Leu	Arg	Gln	Lys	Thr	Met	Arg	Arg	Ala	Gly	Thr	Ile	Arg
65					70					75				80	
Lys	Gln	Arg	Asp	Lys	Leu	Ile	Lys	Glu	Gly	Lys	Tyr	Thr	Pro	Pro	Pro
			85						90					95	
His	His	Ile	Gly	Lys	Gly	Glu	Pro	Arg	Pro						
			100					105							

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTAGTCGT	TCTGAAGCGG	CGGCCAGAGA	AGAGTCAAGG	GCACGAGCAT	CGGCCATGCC	60
TTTCTTGGAC	ATCCAGAAAA	GGTTCGGCCT	TAACATAGAT	CGATGGTTGA	CAATCCAGAG	120
TGGTGAACAG	CCCTACAAGA	TGGCTGGTCG	ATGCCATGCT	TTTGAAAAAG	AATGGATAGA	180
ATGTGCACAT	GGAATCGGTT	ATACTCGGGC	AGAGAAAGAG	TGCAAGATAG	AATATGATGA	240
TTTCGTAGAG	TGTTTGCTTC	GGCAGAAAAC	GATGAGACGT	GCAGGTACCA	TCAGGAAGCA	300
GCGGGATAAG	CTGATAAAGG	AAGGAAAGTA	CACCCCTCCA	CCTCACCACA	TTGGCAAGGG	360
GGAGCCTCGG	CCCTGAACAG	AGCAGCTGCT	GATGTCTGGA	GGCTGATTTT	CCTGTTCTCT	420
GTTCTCCACT	GGAAAGGTTG	TTTACGACAA	ACCTCCTTGT	CAAAGTGTGT		470

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: Consensus
 (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Ile Ala Arg Arg Asn Pro Glu Pro Leu Arg Phe Leu Pro Asp Glu
 1           5           10           15
Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr
 20           25           30
Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg
 35           40           45
Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Xaa Xaa Tyr Ile
 50           55           60
Thr Ala Phe Phe Phe Ala Gly Tyr Tyr Xaa Val Lys Arg Glu Asp Tyr
 65           70           75           80
Leu Tyr Ala Val Arg Asp Arg Glu Met Phe Gly Tyr Met Lys Leu His
 85           90           95
Pro Glu Asp Phe Pro Glu Glu Asp Lys Lys Thr Tyr Gly Glu Ile Phe
100           105           110
Glu Lys Phe His Pro Ile Arg
115
  
```

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: Consensus
 (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

CGCAGAGGAG GAGGAGAAAG CTGACCGCTT AGGCCCGGGT AGTGGTCGTC GTGGTTTTC 60
TTGTAGTTCG TGGTCTGAGA CCAGGCCTCA AGTGGAACG GCGTCACCAT GATCGCACGG 120
CGGAACCCAG AACCCCTACG GTTCTGCCG GATGAGGCC GGAGCCTGCC CCCGCCCAAG 180
CTGACCGACC CGCGGCTCCT CTACATCGGC TTCTTGGGCT ACTGCTCCGG CCTGATTGAT 240
AACCTGATCC GCGGAGGCC GATCGCGACG GCTGGTTTGC ATCGCCAGNT TNTATATATT 300
ACGGCCTTTT TTTTGTCTGG ATATTATNTT GTAAAACGTG AAGACTACCT GTATGCTGTG 360
AGGGACCGTG AAATGTTTGG ATATATGAAA TTACATCCAG AGGATTTTCC TGAAGAAGAT 420
AAGAAAACAT ATGGTGAAAT TTTTGAAAAA TTCCATCCAA TACGTTGAAG TCTTCAAAAT 480
GCTTGCTCCA GTTTCCTGA TACCTGCTGT TTCTGAATTT GATGGAACAT GTTCTTTATG 540
ACAGTTGAAG CTTATGCTAA TCTGTATGTT GACACC 576
  
```

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 163416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Ala Ala Ala Val Ala Ala Ala Ala Pro Gly Cys Trp Gln Arg Leu
1      5      10
Val Gly Ser Ala Ala Pro Ala Arg Val Ala Gly Arg Pro Ser Val Leu
20     25     30
Leu Leu Pro Val Arg Arg Glu Ser Ser Ala Ala Asp Thr Arg Pro Thr
35     40     45
Val Arg Pro Arg Asn Asp Val Ala His Lys Gln Leu Ser Ala Phe Gly
50     55     60
Glu Tyr Val Ala Glu Ile Leu Pro Lys Tyr Val Gln Gln Val Gln Val
65     70     75     80
Ser Cys Phe Asn Glu Leu Glu Ile Cys Ile His Pro Asp Gly Val Ile
85     90     95
Pro Val Leu Thr Phe Leu Arg Asp His Ser Asn Ala Gln Phe Lys Ser
100    105    110
Leu Ala Asp Leu Thr Ala Val Asp Ile Pro Thr Arg Gln Asn Arg Phe
115    120    125
Glu Ile Val Tyr Asn Leu Leu Ser Leu Arg Phe Asn Ser Arg Ile Arg
130    135    140
Val Lys Thr Tyr Thr Asp Glu Leu Thr Pro Ile Glu Ser Ser Val Pro
145    150    155    160
Val Tyr Lys Ala Ala Asn Trp Tyr Glu Arg Glu Ile Trp Asp Met Phe
165    170    175
Gly Val Phe Phe Ala Asn His Pro Asp Leu Arg Arg Ile Leu Thr Asp
180    185    190
Tyr Gly Phe Glu Gly His Pro Phe Arg Lys Asp Phe Pro Leu Ser Gly
195    200    205
Tyr Val Glu Leu Arg Tyr Asp Asp Glu Val Lys Arg Val Val Ala Glu
210    215    220
Pro Val Glu Leu Ala Gln Glu Phe Arg Lys Phe Asp Leu Asn Ser Pro
225    230    235    240
Trp Glu Ala Phe Pro Ala Tyr Arg Gln Pro Pro Glu Ser Leu Lys Leu
245    250    255
Glu Ala Gly Asp Thr Lys Pro Glu Ala Lys
260    265

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Ser Phe Pro Lys Tyr Glu Ala Ser Arg Leu Ser Ser Leu Pro Thr
1      5      10
Thr Leu Asp Pro Ala Glu Tyr Asp Ile Ser Ser Glu Thr Arg Lys Ala
20     25     30
Gln Ala Glu Arg Leu Ala Ile Arg Ser Arg Leu Lys Arg Glu Tyr Gln
35     40     45
Leu Gln Tyr Tyr Asp Pro Ser Arg Arg Gly Val Ile Glu Asp Pro Ala
50     55     60
Leu Val Arg Trp Thr Tyr Ala Arg Ser Ala Asn Ile Tyr Pro Asn Phe
65     70     75     80
Arg Pro Asn Thr Lys Thr Ser Leu Leu Gly Ala Leu Phe Gly Ile Gly
85     90     95

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Pro Leu Val Phe Trp Tyr Tyr Val Phe Lys Thr Asp Arg Asp Arg Lys
100 105 110
Glu Lys Leu Ile Gln Glu Gly Lys Leu Asp Arg Thr Phe Asn Ile Ser
115 120 125
Tyr

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Pro Phe Phe Asp Val Gln Lys Arg Leu Gly Val Asp Leu Asp Arg
1 5 10 15
Trp Met Thr Ile Gln Ser Ala Glu Gln Pro His Lys Ile Pro Ser Arg
20 25 30
Cys His Ala Phe Glu Lys Glu Trp Ile Glu Cys Ala His Gly Ile Gly
35 40 45
Ser Ile Arg Ala Glu Lys Glu Cys Lys Ile Glu Phe Glu Asp Phe Arg
50 55 60
Glu Cys Leu Leu Arg Gln Lys Thr Met Lys Arg Leu His Ala Ile Arg
65 70 75 80
Arg Gln Arg Glu Lys Leu Ile Lys Glu Gly Lys Tyr Thr Pro Pro Pro
85 90 95
His His Ser Gly Gln Glu Glu Pro Arg Ser
100 105

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Met Thr Gly Arg Gln Gly Arg Ala Thr Phe Gln Phe Leu Pro Asp
1 5 10 15
Glu Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Ala
20 25 30
Phe Val Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Ala Ile
35 40 45
Arg Arg Arg Pro Val Leu Leu Ala Gly Leu His Arg Gln Leu Leu Tyr
50 55 60
Ile Thr Ser Phe Val Phe Val Gly Tyr Tyr Leu Leu Lys Arg Gln Asp
65 70 75 80
Tyr Met Tyr Ala Val Arg Asp His Asp Met Phe Ser Tyr Ile Lys Ser

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				85					90					95	
His	Pro	Glu	Asp	Phe	Pro	Glu	Lys	Asp	Lys	Lys	Thr	Tyr	Gly	Glu	Val
			100					105					110		
Phe	Glu	Glu	Phe	His	Pro	Val	Arg								
		115					120								